



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 156085

TO: Sarvamangala Devi
Art Unit: 1645
Location: REM 3C18
Serial Number: 09/964858

Friday, June 10, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

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OM protein - protein search, using sw model

Run on: June 8, 2005, 15:52:15, Search time 162 seconds

(without alignments)
627.889 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263
Perfect score: 1386
Sequence: 1 MNSTPSKLLPDKSHLQ.....NNNEVNSPRLTMDLKR 263

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1386	100.0	1664	AAW99462	AAW99462 C.albican
2	1386	100.0	1664	AAE19799	AAE19799 Candida a
3	1386	100.0	1664	AAU79331	AAU79331 Candida a
4	1386	100.0	1664	ADC73265	ADC73265 Yeast Int
5	1378	99.4	1664	ADM33264	ADM33264 Candida a
6	241	17.4	236	AAW99456	AAW99456 Amino aci
7	241	17.4	236	AAE19800	AAE19800 Candida a
8	241	17.4	236	ADM33265	ADM33265 Candida a
9	139.5	10.1	1166	ABJ18982	ABJ18982 Pathogen
10	138.5	10.0	1166	AAW08643	AAW08643 S. aureus
11	137.5	9.9	371	ABG93277	ABG93277 C. albica
12	134.5	9.7	1133	AAE35697	AAE35697 Human Mas
13	134.5	9.7	1133	ADC59316	ADC59316 Human pol
14	134.5	9.7	1138	ABU05434	ABU05434 Human bre
15	134	9.7	1141	ABU42327	ABU42327 Protein e
16	133	9.6	767	ABBS8240	ABBS8240 Drosophi
17	133	9.6	971	AAW48896	AAW48896 Candida a
18	131.5	9.5	1174	AAE85039	AAE85039 Shrimp wh
19	131.5	9.5	2439	ABE68896	ABE68896 Drosophi
20	128	9.2	618	ADL33450	ADL33450 Lolium pe
21	127.5	9.2	1335	ABP38871	ABP38871 Staphyloc
22	127.5	9.2	1335	ABJ19029	ABJ19029 Pathogen
23	127.5	9.2	1335	ADSO6472	ADSO6472 Staphyloc
24	127.5	9.2	1542	ABB71456	ABB71456 Drosophi
25	127	9.2	4134	AAJ31946	AAJ31946 Plasmodiu

26	126	9.1	1817	3	AAE42230	AAE42230 Human ORF
27	125	9.0	722	4	ABE63899	ABE63899 Drosophi
28	125	9.0	1545	4	ABE65577	ABE65577 Drosophi
29	124.5	9.0	811	4	ABE62661	ABE62661 Drosophi
30	124	8.9	1798	4	ABE71695	ABE71695 Human tra
31	124	8.9	2781	3	AAE57453	AAE57453 Human tra
32	124	8.9	2781	8	ADP42724	ADP42724 Human BPT
33	124	8.9	2781	8	ADQ18653	ADQ18653 Human BPT
34	123	8.9	672	4	AAW93543	AAW93543 Human pol
35	123	8.9	672	8	ADL31262	ADL31262 Human pro
36	123	8.9	874	4	ABE62601	ABE62601 Drosophi
37	123	8.9	1080	5	ABG93254	ABG93254 C. albica
38	123	8.9	1139	6	ABU35640	ABU35640 Protein e
39	123	8.9	1139	7	ABO23514	ABO23514 Mycoplasma
40	123	8.9	1557	4	ABE63735	ABE63735 Drosophi
41	123	8.9	1616	6	ABU35669	ABU35669 Protein e
42	123	8.9	1616	6	ABO23515	ABO23515 Mycoplasma
43	123	8.9	4019	4	AAE13839	AAE13839 Human lun
44	123	8.9	4019	7	ADDE6733	ADDE6733 Human lun
45	123	8.9	4019	7	ADDE7987	ADDE7987 Human lun

ALIGNMENTS

RESULT 1	AAW99462 standard; protein, 1664 AA.
ID	AAW99462
XX	AAW99462;
AC	08-JUN-1999 (first entry)
DT	
XX	
DE	C.albicans alpha-INT1p protein.
XX	
KM	Integrin-like motif; vaccine; immune response; antibody; inhibition;
KW	adhesion; endothelial cell; pathogenesis; infection; probe.
XX	
OS	Candida albicans.
XX	
PN	US586151-A.
PD	23-MAR-1999.
XX	
PP	03-MAY-1996; 96US-00642846.
XX	
PR	03-MAY-1996; 96US-00642846.
XX	
PA	(MINT) UNIV MINNESOTA.
XX	
PI	Tao N, Kendrick K, Gale CA, Hostetter MK, Bendel CW,
XX	WPI; 1999-242618/20.
DR	N-PSDB; AAX25885.
XX	
XX	New isolated Candida albicans protein with integrin-like motifs.
PT	Example; Col 13-14; 21pp; English.
XX	
PS	
XX	This sequence represents the Candida albicans alpha-INT1 protein which
CC	contains integrin-like motifs. The protein was used to derive peptides
CC	AAW99456-W99461 used for producing vaccines for stimulating an immune
CC	response. The antibodies can inhibit the adhesion of C.albicans to cells,
CC	particularly endothelial cells. This blocking activity of the adhesion to
CC	cells can reduce or prevent subsequent events in the pathogenesis of
CC	invasive candidal infection
XX	
XX	Sequence 1664 AA;
XX	
XX	Query Match 100.0%; Score 1386; DB 2; Length 1664;
XX	Best Local Similarity 100.0%; Pred.No. 9.3e-107; Indels 0; Gaps 0;
XX	Matches 263; Conservative 0; Mismatches 0;

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OM protein - protein search, using sw model

Run on: June 8, 2005, 16:21:02 / Search time 173 Seconds
(without alignments)
778.479 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263

Perfect score: 263
Sequence: 1 MNSYPSKLLPDKSHSLQLQ.....KNNNEVSEPALTMKLR 263

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database: 1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	263	100.0	1664	1 INT1 CANAL	P53705 candida alb
2	11	4.2	840	2 O6CHBO	O6chbo yarrowia li
3	11	4.2	2123	2 O9U987	O9u987 dictyostell
4	11	4.2	2189	2 O7SB06	O7sb06 dictyostell
5	10	3.8	31	2 O64LJ3	O64lj3 pongo pygma
6	10	3.8	58	2 O9V8P4	O9v8p4 dictyostell
7	10	3.8	210	2 O86127	O86127 dictyostell
8	10	3.8	224	2 O7PRM3	O7prm3 anophelae g
9	10	3.8	225	2 O9C1A4	O9c1a4 trichophyto
10	10	3.8	247	2 O86YX1	O86yx1 dictyostell
11	10	3.8	255	1 LPE1 SIMTR	P15714 elmeria ten
12	10	3.8	271	2 O7PEH6	O7peh6 anophelae g
13	10	3.8	279	2 O35846	O35846 mus musculu
14	10	3.8	286	1 MCM1 YEAST	P11746 saccharomyc
15	10	3.8	320	2 O7SG91	O7sg91 neurospora
16	10	3.8	333	2 O9W0N1	O9w0n1 dictyostell
17	10	3.8	337	2 O6V744	O6v744 vibrio para
18	10	3.8	353	2 O66116	O66116 dictyostell
19	10	3.8	355	2 O6VSK6	O6vsk6 dictyostell
20	10	3.8	359	2 O9UAF7	O9uaf7 branchiosto
21	10	3.8	360	2 O77158	O77158 branchiosto
22	10	3.8	362	2 O64OM3	O64om3 mus musculu
23	10	3.8	363	1 TOB1 MOUSE	O61471 mus musculu
24	10	3.8	373	2 O6CF10	O6cf10 yarrowia li
25	10	3.8	411	2 O8MU88	O8mu88 strongyloce
26	10	3.8	443	2 O86NLS	O86nls dictyostell
27	10	3.8	447	2 O7PQ39	O7pq39 anophelae g
28	10	3.8	448	1 AAC2 DICDI	P14196 dictyostell
29	10	3.8	464	2 O6H971	O6h971 antirrhinum
30	10	3.8	486	2 O6CDX5	O6cdx5 yarrowia li
31	10	3.8	490	2 O811G0	O811g0 dictyostell

32	10	3.8	536	2 O9P466	O9p466 neurospora
33	10	3.8	550	1 CCF DROME	P41046 dictyostell
34	10	3.8	550	2 O9VN76	O9vn76 dictyostell
35	10	3.8	555	2 O869R1	O869r1 dictyostell
36	10	3.8	572	2 O95BN1	O95bn1 dictyostell
37	10	3.8	578	2 O86P22	O86p22 dictyostell
38	10	3.8	581	2 O18349	O18349 dictyostell
39	10	3.8	582	2 O9VNH2	O9vnh2 dictyostell
40	10	3.8	609	2 O7KSW2	O7ksw2 dictyostell
41	10	3.8	622	2 O7SAK7	O7sak7 dictyostell
42	10	3.8	628	2 O9VSB3	O9vsb3 dictyostell
43	10	3.8	639	2 O7SHN2	O7shn2 neurospora
44	10	3.8	648	1 KAPC DICDI	P34039 dictyostell
45	10	3.8	648	2 O9TXB8	O9txb8 dictyostell
46	10	3.8	661	2 O960R6	O960r6 dictyostell
47	10	3.8	662	2 O780R1	O780r1 dictyostell
48	10	3.8	675	2 O9Y110	O9y110 dictyostell
49	10	3.8	682	2 O86K87	O86k87 dictyostell
50	10	3.8	707	2 O00910	O00910 dictyostell
51	10	3.8	716	2 O7KRB6	O7krb6 dictyostell
52	10	3.8	717	1 ARA DROME	O24248 dictyostell
53	10	3.8	724	2 O868B9	O868b9 anophelae g
54	10	3.8	738	2 O06628	O06628 saccharomyc
55	10	3.8	745	2 O8X0W4	O8x0w4 neurospora
56	10	3.8	756	2 O86PD9	O86pd9 dictyostell
57	10	3.8	759	2 O9VK09	O9vk09 dictyostell
58	10	3.8	772	2 O86P40	O86p40 dictyostell
59	10	3.8	789	2 O86AC9	O86ac9 dictyostell
60	10	3.8	791	1 CUDA DICDI	O00841 dictyostell
61	10	3.8	796	2 O7JPS0	O7jps0 dictyostell
62	10	3.8	797	2 O9V7U9	O9v7u9 dictyostell
63	10	3.8	797	2 O7KRX3	O7kxr3 dictyostell
64	10	3.8	800	2 O915S1	O915s1 xenopus lae
65	10	3.8	806	2 O96828	O96828 dictyostell
66	10	3.8	812	2 O75JL6	O75jl6 dictyostell
67	10	3.8	815	2 O80XQ2	O80xq2 mus musculu
68	10	3.8	816	2 O86HD8	O86hd8 dictyostell
69	10	3.8	833	2 O76P07	O76p07 dictyostell
70	10	3.8	836	2 O784H0	O784h0 neurospora
71	10	3.8	836	2 O81P74	O81p74 dictyostell
72	10	3.8	836	2 O8MCP0	O8mcp0 dictyostell
73	10	3.8	837	2 O86N70	O86n70 dictyostell
74	10	3.8	854	2 O801P6	O801p6 xenopus lae
75	10	3.8	865	2 O91YX8	O91yx8 spalax juda
76	10	3.8	865	2 O91YB0	O91yb0 spalax galli
77	10	3.8	865	2 O91YB2	O91yb2 spalax carm
78	10	3.8	878	2 O81NR4	O81nr4 dictyostell
79	10	3.8	889	2 O8MLW9	O8mlw9 dictyostell
80	10	3.8	893	2 O8MNS5	O8mns5 dictyostell
81	10	3.8	916	2 O6CF23	O6cf23 yarrowia li
82	10	3.8	918	2 O81P76	O81p76 dictyostell
83	10	3.8	926	2 O9W3G1	O9w3g1 dictyostell
84	10	3.8	979	2 O7KWS3	O7kws3 dictyostell
85	10	3.8	981	2 O8M011	O8m011 dictyostell
86	10	3.8	993	2 O7SD03	O7sd03 neurospora
87	10	3.8	1019	2 O6ZS23	O6zs23 homo sapien
88	10	3.8	1024	2 O6PJG2	O6pjg2 homo sapien
89	10	3.8	1024	2 O6PK13	O6pk13 homo sapien
90	10	3.8	1024	2 O86BG2	O86bg2 dictyostell
91	10	3.8	1036	2 O6PKS9	O6pks9 homo sapien
92	10	3.8	1080	1 HDC DROME	O9zn88 dictyostell
93	10	3.8	1180	2 O7JF26	O7jf26 dictyostell
94	10	3.8	1186	2 O9VBD3	O9vbd3 dictyostell
95	10	3.8	1206	1 BUN2 DROME	O24523 dictyostell
96	10	3.8	1208	2 O86HFS	O86hfs dictyostell
97	10	3.8	1230	2 O9GUS3	O9gus3 dictyostell
98	10	3.8	1260	2 O9U9Y9	O9u9y9 homo sapien
99	10	3.8	1271	2 O86123	O86123 dictyostell
100	10	3.8	1319	1 MNI HUMAN	O10571 homo sapien
101	10	3.8	1324	2 O6C0X9	O6c0x9 kluyveromyc
102	10	3.8	1358	2 O7RW22	O7rw22 neurospora
103	10	3.8	1365	1 SUT2 DROME	P25172 dictyostell
104	10	3.8	1368	2 O9V6J0	O9v6j0 dictyostell

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OM protein - protein search, using sw model

Run on: June 8, 2005, 16:12:52 / Search time 41 seconds
(without alignments)
617.195 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263

Perfect score: 263
Sequence: 1 NMSTPSKLLPIDKSHLQD.....NNKNVNSPRLTDMKLR 263

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Selecting first 1000 summaries

Database : PIR 79: *
1: pirl: *
2: pirl2: *
3: pirl3: *
4: pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	263	100.0	1664	2 T18216	integrin-like prot
2	10	3.8	255	2 A60637	mezozone antigen
3	10	3.8	286	2 A34599	DNA-binding protei
4	10	3.8	448	2 S05355	hypothetical prote
5	10	3.8	648	1 JQ1150	protein kinase (BC
6	10	3.8	738	2 S59842	probable membrane
7	10	3.8	800	2 T51653	derRNA-binding prot
8	10	3.8	806	2 T13690	hypothetical prote
9	10	3.8	1180	2 S69205	stripte a/b protein
10	10	3.8	1212	2 T13804	shs protein - fruit
11	10	3.8	1365	2 S14871	suppressor two of
12	10	3.8	1390	2 T14004	trif protein - all
13	10	3.8	1655	2 T13998	gene matetmind pr
14	10	3.8	2715	2 T13049	eyelid - fruit fly
15	10	3.4	104	2 T29540	hypothetical prote
16	9	3.4	154	2 T06508	glutinin low molec
17	9	3.4	473	2 T09580	hypothetical prote
18	9	3.4	488	2 A55180	homeotic protein H
19	9	3.4	597	2 T51889	transcription fact
20	9	3.4	644	2 S39356	eye cell developm
21	9	3.4	760	2 A45174	penicillin-binding
22	9	3.4	846	2 S57580	hypothetical prote
23	9	3.4	1026	2 T20369	C-terminal domain
24	9	3.4	1048	2 T31425	hypothetical prote
25	9	3.4	1271	2 T24008	eye development pr
26	9	3.0	1893	2 A56158	hypothetical prote
27	8	3.0	268	2 T04966	hypothetical prote
28	8	3.0	288	2 T06662	hypothetical prote
29	8	3.0	303	2 T06981	low-molecular-weig

30	8	3.0	304	2 T06505	glutinin low molec
31	8	3.0	323	2 T06506	glutinin low molec
32	8	3.0	355	2 T24010	hypothetical prote
33	8	3.0	394	2 S26492	homeotic protein A
34	8	3.0	399	2 T40831	probable guanine n
35	8	3.0	411	2 T29475	hypothetical prote
36	8	3.0	428	2 F96782	hypothetical prote
37	8	3.0	444	2 A43481	CCAR/enhancer-bin
38	8	3.0	476	2 A39621	homeotic protein H
39	8	3.0	484	2 S44739	CO2C2.1 protein -
40	8	3.0	534	2 T15141	hypothetical prote
41	8	3.0	551	2 F70684	hypothetical prote
42	8	3.0	551	2 S66701	probable membrane
43	8	3.0	592	2 T21536	hypothetical prote
44	8	3.0	613	2 S48557	hypothetical prote
45	8	3.0	625	2 T50992	hypothetical prote
46	8	3.0	632	2 T48316	hypothetical prote
47	8	3.0	643	2 S55610	polypeptide - equi
48	8	3.0	654	2 T30136	hypothetical prote
49	8	3.0	684	2 A56154	Abi substrate ena
50	8	3.0	730	2 A75486	hypothetical prote
51	8	3.0	738	2 S37876	glutamine-rich pro
52	8	3.0	779	2 T20654	hypothetical prote
53	8	3.0	788	2 T25061	hypothetical prote
54	8	3.0	806	2 S22765	heterogeneous ribo
55	8	3.0	873	2 B53225	ecdysone-induced p
56	8	3.0	875	1 T00106	3',5'-cyclic-GMP p
57	8	3.0	904	2 G64840	protein-histidine
58	8	3.0	933	2 F86427	auxin response fac
59	8	3.0	992	2 A42318	glycogen phosphory
60	8	3.0	1004	2 H88562	protein C07A5.3 f1
61	8	3.0	1044	2 S40704	hypothetical prote
62	8	3.0	1088	2 H86747	unknown protein T1
63	8	3.0	1102	2 T39943	hypothetical prote
64	8	3.0	1198	2 T49726	hypothetical prote
65	8	3.0	1209	2 T31153	ecdysone-associated
66	8	3.0	1237	2 A34598	brachma associated
67	8	3.0	1314	1 TMBYR6	neurogenic locus m
68	8	3.0	1480	2 S48440	hypothetical prote
69	8	3.0	1558	2 C89114	SNF2alpha protein
70	8	3.0	1572	2 S45251	hypothetical prote
71	8	3.0	1596	2 A33106	hypothetical prote
72	8	3.0	2027	2 S60123	hypothetical prote
73	8	3.0	2056	2 G88564	protein R10E1.1 f
74	8	3.0	2167	2 T34395	hypothetical prote
75	8	2.7	111	2 B30102	GTP-binding protei
76	7	2.7	110	2 T49553	hypothetical prote
77	7	2.7	120	2 G82653	HCB-related prote
78	7	2.7	125	2 S80762	probable regulator
79	7	2.7	132	2 S56255	hypothetical prote
80	7	2.7	172	1 D31482	H+-transporting tw
81	7	2.7	183	2 D90335	terminal quinol ox
82	7	2.7	206	2 S44894	ZK1236.6 protein -
83	7	2.7	206	2 S61705	hypothetical prote
84	7	2.7	207	2 S32124	B2 protein - carro
85	7	2.7	213	2 T23865	hypothetical prote
86	7	2.7	223	2 S16269	auxin-induced prote
87	7	2.7	223	2 S16268	glutelin low molec
88	7	2.7	229	2 S7654	glutelin low molec
89	7	2.7	234	2 D96592	hypothetical prote
90	7	2.7	239	2 C88395	protein P53A3.4 f1
91	7	2.7	243	2 T27493	hypothetical prote
92	7	2.7	244	2 S07398	gamma-glutadin B pr
93	7	2.7	250	2 C86429	hypothetical prote
94	7	2.7	261	2 T00747	histone H1-I - Vol
95	7	2.7	261	2 S57655	glutelin low molec
96	7	2.7	267	1 S30863	BMI protein - yea
97	7	2.7	267	2 T15645	hypothetical prote
98	7	2.7	276	2 S57656	glutelin low molec
99	7	2.7	281	2 T04295	heat-shock protein
100	7	2.7	285	2 S20853	glutelin low molec
101	7	2.7	286	2 T05910	glutelin low molec
102	7	2.7	295	1 T06636	glutelin low molec

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OW protein - protein search, using SW model

Run on: June 8, 2005, 16:28:54 / Search time 157 Seconds
(without alignments)
642.146 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263

Perfect score: 263
Sequence: 1 MNSTPSKLPIDKSHLQLO.....NKNNEVSEPALTDMLKFR 263

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1710399 seqs, 38334425 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

Published Applications AA:
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2: /cgm2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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6: /cgm2_6/ptodata/2/pubpaa/PCTUS_NEW_PUB.pep.*
7: /cgm2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgm2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgm2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgm2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgm2_6/ptodata/2/pubpaa/US09C_NEW_PUB.pep.*
13: /cgm2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgm2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
17: /cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
18: /cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
19: /cgm2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgm2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	263	100.0	1664	10	US-09-978-343-2
2	263	100.0	1664	10	US-09-964-858a-1
3	46	17.5	236	10	US-09-978-343-1
4	15	5.7	15	10	US-09-964-858a-4
5	11	4.2	659	16	US-10-425-115-189446
6	10	3.8	9	16	US-10-856-499-653
7	10	3.8	181	15	US-10-424-599-159517
8	10	3.8	286	9	US-09-801-368-188
9	10	3.8	286	16	US-10-451-467A-306
10	10	3.8	295	15	US-10-424-599-272882
11	10	3.8	406	15	US-10-369-493-3147

12	10	3.8	427	16	US-10-425-115-258112	Sequence 258112, A
13	10	3.8	648	17	US-10-732-923-10742	Sequence 10742, A
14	10	3.8	743	14	US-10-278-703-4	Sequence 4, Appl1
15	10	3.8	743	15	US-10-380-334-4	Sequence 4, Appl1
16	10	3.8	797	14	US-10-032-585-7208	Sequence 7208, Ap
17	10	3.8	920	13	US-10-087-192-1518	Sequence 1518, Ap
18	10	3.8	1038	9	US-09-752-639-151	Sequence 151, App
19	10	3.8	1038	9	US-09-984-198-151	Sequence 151, App
20	10	3.8	1038	17	US-10-967-092-151	Sequence 151, App
21	10	3.8	1319	16	US-10-732-923-866-2204	Sequence 2204, Ap
22	10	3.8	1358	16	US-10-778-804-11	Sequence 11, Appl
23	10	3.8	1692	15	US-10-432-422-41	Sequence 41, Appl
24	9	3.4	149	16	US-10-425-115-349865	Sequence 349865, A
25	9	3.4	265	9	US-09-960-253-185	Sequence 185, App
26	9	3.4	275	15	US-10-424-599-184082	Sequence 184082, A
27	9	3.4	307	16	US-10-732-923-8889	Sequence 8889, Ap
28	9	3.4	328	15	US-10-424-599-203656	Sequence 203656, A
29	9	3.4	345	9	US-09-943-846-2	Sequence 846, App
30	9	3.4	345	16	US-10-648-599-210	Sequence 210, App
31	9	3.4	345	16	US-10-739-043-2	Sequence 2, Appl1
32	9	3.4	351	15	US-10-334-143-53	Sequence 53, Appl
33	9	3.4	353	9	US-09-925-297-814	Sequence 814, App
34	9	3.4	503	15	US-10-424-599-211275	Sequence 211275, A
35	9	3.4	548	16	US-10-767-701-44506	Sequence 44506, A
36	9	3.4	568	17	US-10-732-923-13759	Sequence 13759, A
37	9	3.4	580	17	US-10-732-923-13758	Sequence 13758, A
38	9	3.4	586	16	US-10-425-115-327159	Sequence 327159, A
39	9	3.4	712	17	US-10-732-923-17486	Sequence 17486, A
40	9	3.4	717	15	US-10-425-114-66724	Sequence 66724, A
41	9	3.4	752	13	US-10-108-605-133	Sequence 133, App
42	9	3.4	752	14	US-10-190-012-29	Sequence 29, Appl
43	9	3.4	752	17	US-10-689-576-29	Sequence 29, Appl
44	9	3.4	760	8	US-08-754-118-2	Sequence 2, Appl1
45	9	3.4	769	16	US-10-737-965-181417	Sequence 181417, A
46	9	3.4	1026	17	US-10-415-656-2	Sequence 2, Appl1
47	9	3.4	1257	17	US-10-741-849-7141	Sequence 7141, Ap
48	9	3.4	1736	16	US-10-437-963-188684	Sequence 188684, A
49	9	3.4	2017	15	US-10-114-270-86	Sequence 86, Appl
50	8	3.0	44	9	US-09-864-761-40491	Sequence 40491, A
51	8	3.0	80	16	US-10-425-115-260679	Sequence 260679, A
52	8	3.0	87	15	US-10-424-599-166633	Sequence 166633, A
53	8	3.0	93	15	US-10-424-599-222192	Sequence 222192, A
54	8	3.0	94	16	US-10-425-115-215073	Sequence 215073, A
55	8	3.0	102	5	US-10-424-599-201710	Sequence 201710, A
56	8	3.0	105	9	US-09-738-626-5146	Sequence 5146, Ap
57	8	3.0	131	16	US-10-425-115-273011	Sequence 273011, A
58	8	3.0	145	15	US-10-425-115-352152	Sequence 352152, A
59	8	3.0	161	15	US-10-424-599-276405	Sequence 276405, A
60	8	3.0	161	16	US-10-425-115-258459	Sequence 258459, A
61	8	3.0	166	16	US-10-425-115-359397	Sequence 359397, A
62	8	3.0	186	15	US-10-425-114-67430	Sequence 67430, A
63	8	3.0	189	16	US-10-739-930-8830	Sequence 8830, Ap
64	8	3.0	208	9	US-09-864-761-36456	Sequence 36456, A
65	8	3.0	219	15	US-10-094-744-2381	Sequence 2381, Ap
66	8	3.0	275	15	US-10-425-114-38694	Sequence 38694, A
67	8	3.0	292	16	US-10-451-467A-486	Sequence 486, App
68	8	3.0	300	15	US-10-424-599-186521	Sequence 186521, A
69	8	3.0	303	16	US-10-437-963-116439	Sequence 116439, A
70	8	3.0	304	16	US-10-739-930-9778	Sequence 9778, Ap
71	8	3.0	310	16	US-10-821-273-80	Sequence 80, Appl
72	8	3.0	313	17	US-10-774-355A-1568	Sequence 1568, Ap
73	8	3.0	341	16	US-10-739-930-9636	Sequence 9636, Ap
74	8	3.0	346	15	US-10-737-963-134252	Sequence 134252, A
75	8	3.0	346	16	US-10-424-599-159122	Sequence 159122, A
76	8	3.0	348	15	US-10-425-114-37391	Sequence 37391, A
77	8	3.0	365	16	US-10-469-483-2	Sequence 2, Appl1
78	8	3.0	378	9	US-09-970-711-6	Sequence 6, Appl1
79	8	3.0	419	16	US-10-425-115-288060	Sequence 288060, A
80	8	3.0	485	14	US-10-128-711-3085	Sequence 3085, Ap
81	8	3.0	490	17	US-10-732-923-10715	Sequence 10715, A
82	8	3.0	502	17	US-10-732-923-10716	Sequence 10716, A
83	8	3.0	510	14	US-10-128-711-8085	Sequence 8085, Ap
84	8	3.0	594	15	US-10-425-114-70186	Sequence 70186, A

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OM protein - protein search, using sw model

Run on: June 8, 2005, 16:28:19 ; Search time 42 Seconds

(without alignments)
467,445 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263

Perfect score: 263

Sequence: 1 NUNSTPKRLPIDKSHLQIQ.....NNKNENSRPALTDKLR 263

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
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- 5: /cgn2_6/prodata/1/aa/5C_COMB.pep.*
- 6: /cgn2_6/prodata/1/aa/5D_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	263	100.0	1664	1 US-09-599-652-2	Sequence 2, App11
2	263	100.0	1664	2 US-08-642-846-2	Sequence 2, App11
3	263	100.0	1664	3 US-09-264-604-2	Sequence 2, App11
4	263	100.0	1664	4 US-09-978-943-2	Sequence 2, App11
5	72	27.4	927	4 US-09-248-796A-14284	Sequence 14284, A
6	46	17.5	236	1 US-09-599-652-3	Sequence 3, App11
7	46	17.5	236	2 US-08-642-846-3	Sequence 3, App11
8	46	17.5	236	3 US-09-264-604-3	Sequence 3, App11
9	46	17.5	236	4 US-09-978-943-3	Sequence 3, App11
10	10	3.8	86	4 US-09-248-796A-21968	Sequence 21968, A
11	10	3.8	99	4 US-09-640-211A-653	Sequence 653, App
12	10	3.8	239	4 US-09-248-796A-15289	Sequence 15289, A
13	10	3.8	239	4 US-09-248-796A-17017	Sequence 17017, A
14	10	3.8	236	4 US-09-248-796A-19181	Sequence 19181, A
15	10	3.8	236	4 US-09-248-796A-24866	Sequence 24866, A
16	10	3.8	322	4 US-09-248-796A-23546	Sequence 23546, A
17	10	3.8	448	4 US-09-248-796A-18659	Sequence 18659, A
18	10	3.8	738	4 US-09-538-092-818	Sequence 818, App
19	10	3.8	1038	4 US-09-081-385-151	Sequence 151, App
20	10	3.8	1319	4 US-09-538-092-1291	Sequence 1291, App
21	10	3.8	1343	4 US-09-949-016-10641	Sequence 10641, A
22	9	3.4	35	4 US-09-270-767-60682	Sequence 60682, A
23	9	3.4	136	4 US-09-270-767-57861	Sequence 57861, A
24	9	3.4	268	4 US-09-270-767-42555	Sequence 42555, A
25	9	3.4	273	4 US-09-270-767-42116	Sequence 42116, A
26	9	3.4	273	4 US-09-248-796A-20577	Sequence 20577, A
27	9	3.4	345	3 US-08-718-738-2	Sequence 2, App11

28	9	3.4	345	3 US-09-221-844-2	Sequence 2, App11
29	9	3.4	345	4 US-09-843-846-2	Sequence 2, App11
30	9	3.4	345	5 PCT-US95-03323A-2	Sequence 2, App11
31	9	3.4	351	4 US-09-949-016-8079	Sequence 8079, App
32	9	3.4	382	4 US-09-248-796A-18720	Sequence 18720, A
33	9	3.4	393	4 US-09-248-796A-24239	Sequence 24239, A
34	9	3.4	729	3 US-09-625-188-20	Sequence 20, App1
35	9	3.4	752	4 US-08-943-667-29	Sequence 29, App1
36	9	3.4	760	1 US-08-195-152-2	Sequence 2, App11
37	9	3.4	760	4 US-08-754-311B-2	Sequence 2, App11
38	9	3.4	884	4 US-09-248-796A-20574	Sequence 20574, A
39	9	3.4	1268	4 US-09-270-767-45320	Sequence 45320, A
40	8	3.0	92	4 US-09-248-796A-25354	Sequence 25354, A
41	8	3.0	139	4 US-09-248-796A-25405	Sequence 25405, A
42	8	3.0	175	4 US-09-248-796A-18867	Sequence 18867, A
43	8	3.0	190	4 US-09-248-796A-22090	Sequence 22090, A
44	8	3.0	193	4 US-09-248-796A-16441	Sequence 16441, A
45	8	3.0	309	4 US-09-270-767-41965	Sequence 41965, A
46	8	3.0	378	3 US-09-171-461-6	Sequence 6, App11
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48	8	3.0	494	4 US-09-248-796A-14156	Sequence 14156, A
49	8	3.0	535	4 US-09-248-796A-18860	Sequence 18860, A
50	8	3.0	585	4 US-09-196-270-4	Sequence 4, App11
51	8	3.0	593	4 US-09-248-796A-19340	Sequence 19340, A
52	8	3.0	684	4 US-09-823-240A-9	Sequence 9, App11
53	8	3.0	712	4 US-09-248-796A-19645	Sequence 19645, A
54	8	3.0	788	2 US-08-918-914-4	Sequence 4, App11
55	8	3.0	806	1 US-07-980-528-2	Sequence 2, App11
56	8	3.0	824	4 US-09-538-092-1242	Sequence 1242, App
57	8	3.0	855	2 US-08-816-6933A-2	Sequence 2, App11
58	8	3.0	855	3 US-08-885-291-2	Sequence 2, App11
59	8	3.0	855	3 US-09-496-672-2	Sequence 2, App11
60	8	3.0	855	4 US-09-618-425-11	Sequence 11, App1
61	8	3.0	875	1 US-08-480-5478A-23	Sequence 23, App1
62	8	3.0	875	1 US-08-250-8478B-23	Sequence 23, App1
63	8	3.0	875	2 US-08-463-9499A-23	Sequence 23, App1
64	8	3.0	875	2 US-08-464-410A-23	Sequence 23, App1
65	8	3.0	875	3 US-09-226-741-5	Sequence 5, App11
66	8	3.0	875	4 US-09-595-514-5	Sequence 5, App11
67	8	3.0	875	5 PCT-US94-06066-23	Sequence 23, App1
68	8	3.0	928	4 US-09-506-066B-2	Sequence 2, App11
69	8	3.0	945	4 US-09-248-796A-15743	Sequence 15743, A
70	8	3.0	1357	4 US-09-270-767-44971	Sequence 44971, A
71	7	2.7	62	4 US-09-248-796A-23338	Sequence 23338, A
72	7	2.7	65	4 US-09-248-796A-23824	Sequence 23824, A
73	7	2.7	91	4 US-09-248-796A-26462	Sequence 26462, A
74	7	2.7	99	4 US-09-270-767-35416	Sequence 35416, A
75	7	2.7	106	4 US-09-270-767-38438	Sequence 38438, A
76	7	2.7	106	4 US-09-270-767-51655	Sequence 51655, A
77	7	2.7	107	4 US-09-248-796A-16188	Sequence 16188, A
78	7	2.7	110	4 US-09-538-092-468	Sequence 468, App
79	7	2.7	126	4 US-09-248-796A-13808	Sequence 13808, A
80	7	2.7	132	3 US-09-224-505-5	Sequence 5, App11
81	7	2.7	132	3 US-09-224-505-6	Sequence 6, App11
82	7	2.7	135	4 US-09-270-767-34885	Sequence 34885, A
83	7	2.7	135	4 US-09-270-767-50102	Sequence 50102, A
84	7	2.7	138	4 US-09-270-767-31670	Sequence 31670, A
85	7	2.7	138	4 US-09-270-767-55887	Sequence 55887, A
86	7	2.7	138	4 US-09-270-767-55887	Sequence 26039, A
87	7	2.7	138	4 US-09-248-796A-26039	Sequence 26039, A
88	7	2.7	139	4 US-09-248-796A-28716	Sequence 18716, A
89	7	2.7	141	4 US-09-270-767-53933	Sequence 53933, A
90	7	2.7	141	4 US-09-270-767-39774	Sequence 39774, A
91	7	2.7	152	4 US-09-270-767-54991	Sequence 54991, A
92	7	2.7	152	4 US-09-248-796A-21018	Sequence 21018, A
93	7	2.7	154	4 US-09-248-796A-19084	Sequence 19084, A
94	7	2.7	159	4 US-09-248-796A-23424	Sequence 23424, A
95	7	2.7	176	4 US-09-270-767-43574	Sequence 43574, A
96	7	2.7	189	4 US-09-252-9913A-29221	Sequence 29221, A
97	7	2.7	201	3 US-09-080-983-19	Sequence 19, App1
98	7	2.7	205	3 US-08-630-915A-16	Sequence 16, App1
99	7	2.7	205	3 US-08-630-915A-16	Sequence 16, App1
100	7	2.7	205	4 US-09-879-957-16	Sequence 16, App1

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OM protein - protein search, using sw model

Run on: June 8, 2005, 16:11:47, Search time 75 Seconds
(without alignments)
1356,240 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263

Perfect score: 263
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Scoring table: Gapop 60.0, Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: A_Geneseq_15Dec04:*

- 1: geneseqp19808:*
- 2: geneseqp19808:*
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- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	263	100.0	1664	2 AAW99462	AAW99462 C. albican
2	263	100.0	1664	5 AAB19799	AAB19799 Candida a
3	263	100.0	1664	5 AAU79331	AAU79331 Candida a
4	263	100.0	1664	7 ADC73265	ADC73265 Yeast int
5	87	33.1	1664	7 ADM33264	ADM33264 Candida a
6	46	17.5	236	2 AAW99456	AAW99456 Antino aci
7	46	17.5	236	5 AAB19800	AAB19800 Candida a
8	46	17.5	236	5 AAB33265	AAB33265 Candida a
9	16	6.1	16	7 ADC73274	ADC73274 Yeast int
10	15	5.7	15	7 ADC73269	ADC73269 Yeast int
11	15	5.7	15	7 ADC73269	ADC73269 Yeast int
12	10	3.8	58	4 ABB69460	ABB69460 Drosophila
13	10	3.8	60	4 ABB68465	ABB68465 Drosophila
14	10	3.8	99	3 AAB32604	AAB32604 Eucalyptu
15	10	3.8	286	5 AAB30808	AAB30808 Antino aci
16	10	3.8	286	5 AAB30808	AAB30808 Antino aci
17	10	3.8	333	4 ABB68754	ABB68754 Drosophila
18	10	3.8	363	5 ABB68754	ABB68754 Drosophila
19	10	3.8	406	8 AAB20494	AAB20494 Bacteri
20	10	3.8	550	4 ABB59194	ABB59194 Drosophila
21	10	3.8	578	4 ABB58393	ABB58393 Drosophila
22	10	3.8	582	4 ABB71745	ABB71745 Drosophila
23	10	3.8	588	8 ABB48570	ABB48570 Protein 8
24	10	3.8	675	4 ABB62402	ABB62402 Drosophila
25	10	3.8	717	4 ABB71958	ABB71958 Drosophila

26	10	3.8	738	7 ADK63388	ADK63388 Disease c
27	10	3.8	743	5 ABB79410	ABB79410 Candida a
28	10	3.8	743	5 ABB47970	ABB47970 Candida a
29	10	3.8	797	5 ABB64072	ABB64072 Drosophila
30	10	3.8	797	5 ABB73371	ABB73371 Candida a
31	10	3.8	900	4 ABB62018	ABB62018 Drosophila
32	10	3.8	920	7 ABB85701	ABB85701 Human pro
33	10	3.8	926	4 ABB65135	ABB65135 Drosophila
34	10	3.8	1018	8 ABB09537	ABB09537 Human pro
35	10	3.8	1038	7 ABB56511	ABB56511 Human chr
36	10	3.8	1099	7 ABB080166	ABB080166 Human chr
37	10	3.8	1137	4 ABB61503	ABB61503 Drosophila
38	10	3.8	1186	4 ABB63516	ABB63516 Drosophila
39	10	3.8	1246	4 ABB61547	ABB61547 Drosophila
40	10	3.8	1301	4 ABB65129	ABB65129 Drosophila
41	10	3.8	1319	4 ABB40120	ABB40120 Human pol
42	10	3.8	1319	8 ABB75584	ABB75584 Marker ge
43	10	3.8	1319	8 ABB75584	ABB75584 Marker ge
44	10	3.8	1342	4 ABB608234	ABB608234 Novel hum
45	10	3.8	1368	4 ABB60262	ABB60262 Drosophila
46	10	3.8	1419	4 ABB65521	ABB65521 Drosophila
47	10	3.8	1665	4 ABB64010	ABB64010 Drosophila
48	10	3.8	1692	4 ABB03390	ABB03390 Fusarium
49	10	3.8	1692	5 ABB92714	ABB92714 Fusarium
50	10	3.8	1700	4 ABB608232	ABB608232 Novel hum
51	10	3.8	1798	4 ABB71695	ABB71695 Drosophila
52	10	3.8	1848	4 ABB68996	ABB68996 Drosophila
53	10	3.8	2309	4 ABB66232	ABB66232 Drosophila
54	10	3.8	2439	4 ABB68896	ABB68896 Drosophila
55	10	3.8	2703	4 ABB63239	ABB63239 Drosophila
56	10	3.8	2703	5 ABB70019	ABB70019 Larval vi
57	10	3.8	3080	4 ABB64877	ABB64877 Drosophila
58	10	3.4	53	4 ABB69858	ABB69858 Drosophila
59	9	3.4	104	4 ABB67522	ABB67522 Drosophila
60	9	3.4	124	4 ABB13778	ABB13778 Human pol
61	9	3.4	198	4 ABB71093	ABB71093 Drosophila
62	9	3.4	224	4 ABB698522	ABB698522 Drosophila
63	9	3.4	265	5 ABB34150	ABB34150 Human lun
64	9	3.4	296	4 ABB65268	ABB65268 Drosophila
65	9	3.4	345	2 ABB01097	ABB01097 Human B-c
66	9	3.4	345	2 ABB48762	ABB48762 Human B-c
67	9	3.4	345	2 ABB78790	ABB78790 Human B-c
68	9	3.4	345	2 ABB05422	ABB05422 Human B-c
69	9	3.4	345	5 ABB24532	ABB24532 Human pro
70	9	3.4	345	8 ABB61286	ABB61286 Human pro
71	9	3.4	345	8 ABB059616	ABB059616 Human Brg
72	9	3.4	351	7 ABB40946	ABB40946 Novel hum
73	9	3.4	351	8 ABB15666	ABB15666 Kinase 61
74	9	3.4	353	3 ABB54362	ABB54362 Human pan
75	9	3.4	363	4 ABB68590	ABB68590 Drosophila
76	9	3.4	386	4 ABB70522	ABB70522 Drosophila
77	9	3.4	488	8 ABB183722	ABB183722 Human PRO
78	9	3.4	488	8 ABB09664	ABB09664 Human pro
79	9	3.4	506	4 ABB63721	ABB63721 Drosophila
80	9	3.4	640	4 ABB67963	ABB67963 Drosophila
81	9	3.4	644	4 ABB70436	ABB70436 Drosophila
82	9	3.4	729	5 ABB11298	ABB11298 Ashbya go
83	9	3.4	752	4 ABB57927	ABB57927 Drosophila
84	9	3.4	752	4 ABB67127	ABB67127 Drosophila
85	9	3.4	752	4 ABB57782	ABB57782 Drosophila
86	9	3.4	755	4 ABB67126	ABB67126 Drosophila
87	9	3.4	760	2 ABB29490	ABB29490 Programme
88	9	3.4	760	5 ABB75570	ABB75570 Programme
89	9	3.4	766	4 ABB64516	ABB64516 Drosophila
90	9	3.4	941	4 ABB65715	ABB65715 Drosophila
91	9	3.4	941	4 ABB65714	ABB65714 Drosophila
92	9	3.4	1003	4 ABB68762	ABB68762 Drosophila
93	9	3.4	1257	8 ABB98966	ABB98966 C. albica
94	9	3.4	1323	8 ABB735096	ABB735096 Xylanae
95	9	3.4	1543	4 ABB66226	ABB66226 Drosophila
96	9	3.4	1778	4 ABB660081	ABB660081 Drosophila
97	9	3.4	1954	4 ABB59197	ABB59197 Drosophila
98	9	3.4	2017	6 ABB54584	ABB54584 Human NOV

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 8, 2005, 16:01:00 / Search time 40 seconds
(without alignments)
632.625 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263

Perfect score: 1386
Sequence: 1 MNSPSPKLPIDKSHSLQ.....NKNNEVNSPEALTDMLKR 263

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: PIR.79.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1386	100.0	1664	2 T18216	Integrin-like prot
2	141.5	10.2	236	2 B90577	lipoprotein b [imp
3	138.5	10.0	1166	2 T28680	fibrirogen-binding
4	137	9.9	947	2 T08605	hypothetical prote
5	134	9.7	1141	2 B89824	hypothetical prote
6	132	9.5	499	2 B46650	weira protein - Pen
7	130.5	9.4	1380	2 B57150	ZMS1 protein - Yea
8	130	9.4	1087	2 B58147	protein kinase - f
9	128.5	9.3	1159	2 B62562	probable nuclear p
10	127.5	9.2	1335	2 T30211	autolysin B - Stap
11	127	9.2	736	2 T41259	hypothetical prote
12	127	9.2	1338	2 T18416	hypothetical prote
13	125	9.0	309	2 B57102	hypothetical prote
14	125	9.0	646	2 D82433	conserved hypochet
15	124.5	9.0	773	2 P90537	lipoprotein [impor
16	124.5	9.0	3848	2 T17414	T4PC protein - all
17	123.5	8.9	1094	2 B49313	protein kinase - B
18	123.5	8.9	1254	2 T18277	kinasein heavy chai
19	123	8.9	619	2 D90072	hypothetical prote
20	123	8.9	1139	1 B64234	cytadherence-acces
21	123	8.9	1616	2 G64242	cytadherence-acces
22	123	8.9	2541	2 T29340	hypothetical prote
23	121.5	8.8	529	2 T50609	hypothetical prote
24	121.5	8.8	948	2 T24445	hypothetical prote
25	121.5	8.8	6642	2 T29457	protein UNC-89 - C
26	121	8.7	368	2 G88636	protein W09G12.7 [
27	121	8.7	522	2 T40520	hypothetical prote
28	121	8.7	605	2 B48940	hypothetical prote
29	120.5	8.7	910	1 B73361	dmu Homolog prote

30	120.5	8.7	916	2 B22864	DNA topoisomerase
31	120	8.7	844	2 B71944	securin formation p
32	120	8.7	1015	2 T13062	clock protein - fr
33	120	8.7	1457	2 T14577	protein kinase Yak
34	119.5	8.6	599	1 A64325	cytadherence-acces
35	119.5	8.6	872	1 B62061	SCDS protein - yea
36	119	8.6	1186	2 B72229	meiotic recombina
37	118.5	8.5	1390	2 T14004	trfa protein - all
38	118	8.5	411	2 T40538	hypothetical prote
39	118	8.5	462	1 A60746	chromogranin A pre
40	118	8.5	842	2 B60402	protein kinase CLA
41	118	8.5	879	2 B64755	hypothetical prote
42	118	8.5	1089	2 T14576	nosa protein - all
43	117.5	8.5	1274	2 A89959	hypothetical prote
44	117	8.4	1062	2 G86325	hypothetical prote
45	116.5	8.4	630	2 T38023	probable transcrip

ALIGNMENTS

RESULT 1

T18216 Integrin-like protein alpha chain - yeast (Candida albicans)

C/Species: Candida albicans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18216

R/Gale, C.; Finkel, D.; Tao, N.; Melinke, M.; McClellan, M.; Olson, J.; Kendrick, K.; He

Proc. Natl. Acad. Sci. U.S.A. 93, 357-361, 1996

A/Title: Cloning and expression of a gene encoding an Integrin-like protein in Candida a

A/Reference number: 206510, PMID:96133936, PMID:8552638

A/Accession: T18216

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1664 <GAL>

A/Cross-references: UNIPROT:P53705; EMBL:U95070; NID:G1144530; PID:G1144531; PIDN:AAA96

C/Genes:

A/Gene: alpha INT1

Query Match 100.0%; Score 1386; DB 2; Length 1664;
Best Local Similarity 100.0%; Pred. No. 5.2e-80;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNSTPSPKLPIDKSHSLQPOSSASINSPKPNPRTNKRSLDPRSSSDTTTSQ	60
DB	1	MNSTPSPKLPIDKSHSLQPOSSASINSPKPNPRTNKRSLDPRSSSDTTTSQ	60
QY	61	DOEKGRKKKDTAFQTSFDRNPDLDNSIDIQOTIHOQOOOPQOOOOLSGTDNNLIDFSS	120
DB	61	DOEKGRKKKDTAFQTSFDRNPDLDNSIDIQOTIHOQOOOPQOOOOLSGTDNNLIDFSS	120
QY	121	QPMSTLDTLTKONPVDKVENHAFYINTSPNKSIMKKAEPKAPKVAFTVNEIR	180
DB	121	QPMSTLDTLTKONPVDKVENHAFYINTSPNKSIMKKAEPKAPKVAFTVNEIR	180
QY	181	HYDNRVSEEDSQOQKEDSVPEPLIOHWKDSQFNYSDEDTNAAVPPPTPLTTTPTA	240
DB	181	HYDNRVSEEDSQOQKEDSVPEPLIOHWKDSQFNYSDEDTNAAVPPPTPLTTTPTA	240
QY	241	QILNKNNEVNSPEALTDMLKR	263
DB	241	QILNKNNEVNSPEALTDMLKR	263

RESULT 2

B90577 lipoprotein b [imported] - Mycoplasma pulmonis (strain UAB CT1P)

C/Species: Mycoplasma pulmonis

C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C/Accession: B90577

R/Chamand, J.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.

Nucleic Acids Res. 29, 2145-2153, 2001

A/Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul

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OM protein - protein search, using sw model

Run on: June 8, 2005, 16:10:16 ; Search time 158 Seconds
(without alignments)
638.082 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263
Perfect score: 1366
Sequence: 1 NINTEPSPALPDHSHLQ.....NNNNVSEPPALTMKLR 263

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications AA:
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/PCT06_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubppa/US11_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1366	100.0	1664	US-09-978-343-2	Sequence 2, Appl1
2	1386	100.0	1664	US-09-964-858-1	Sequence 1, Appl1
3	241	17.4	236	US-09-978-343-1	Sequence 0, Appl1
4	139.5	10.1	1166	US-10-470-048B-153	Sequence 153, Appl
5	138.5	10.0	1166	US-10-744-672-7	Sequence 7, Appl1
6	138.5	10.0	1166	US-10-744-616-7	Sequence 512, Appl
7	137.5	9.9	371	US-10-451-467A-512	Sequence 194, App
8	134.5	9.7	1138	US-10-074-475-194	Sequence 70251, A
9	134	9.7	1141	US-10-282-122A-70251	Sequence 8, Appl1
10	133	9.6	971	US-10-093-524-8	Sequence 25, Appl1
11	128	9.2	618	US-10-655-799-25	

12	127.5	9.2	1335	17	US-10-470-048B-278	Sequence 278, App
13	124	8.9	2781	15	US-10-263-929-122	Sequence 122, App
14	124	8.9	2781	16	US-10-723-860-1472	Sequence 1472, App
15	123	8.9	1080	16	US-10-451-467A-466	Sequence 466, App
16	123	8.9	1139	10	US-09-820-843A-15	Sequence 15, Appl1
17	123	8.9	1139	15	US-10-282-122A-63564	Sequence 63564, A
18	123	8.9	1616	10	US-09-820-843A-16	Sequence 16, Appl1
19	123	8.9	1616	15	US-10-282-122A-63593	Sequence 63593, A
20	123	8.9	4019	9	US-09-738-973-425	Sequence 425, App
21	123	8.9	4019	9	US-09-854-133-425	Sequence 425, App
22	123	8.9	4019	14	US-10-144-649A-425	Sequence 425, App
23	122.5	8.8	5342	15	US-10-425-114-72709	Sequence 72709, A
24	122.5	8.8	1022	17	US-10-732-923-8729	Sequence 8729, App
25	121.5	8.8	6642	15	US-10-369-493-5013	Sequence 5013, App
26	121	8.7	605	9	US-09-801-368-428	Sequence 428, App
27	121	8.7	605	15	US-10-369-493-22016	Sequence 22016, A
28	121	8.7	619	17	US-10-470-048B-61	Sequence 61, Appl1
29	121	8.7	1213	17	US-10-732-923-12952	Sequence 12952, A
30	120.5	8.7	608	17	US-10-732-923-10720	Sequence 10720, A
31	120	8.7	844	9	US-09-815-242-11497	Sequence 11497, A
32	120	8.7	844	15	US-10-335-977-5799	Sequence 5799, App
33	120	8.7	847	15	US-10-335-977-5800	Sequence 5800, App
34	120	8.7	849	15	US-10-335-977-5801	Sequence 5801, App
35	119.5	8.6	599	15	US-10-335-977-5801	Sequence 5801, App
36	119	8.6	1381	15	US-10-369-493-1940	Sequence 63567, A
37	119	8.6	1381	16	US-10-451-467A-425	Sequence 425, App
38	119	8.6	1920	15	US-10-282-122A-71413	Sequence 71413, A
39	118	8.5	460	16	US-10-767-701-42484	Sequence 42484, A
40	118	8.5	842	15	US-10-369-493-1940	Sequence 1940, App
41	118	8.5	1024	16	US-10-479-546-1	Sequence 12, Appl1
42	118	8.5	1153	15	US-10-479-546-1	Sequence 1, Appl1
43	118	8.5	6641	15	US-10-282-122A-70580	Sequence 70580, A
44	118	8.5	10203	16	US-10-661-809-23	Sequence 23, Appl1
45	117.5	8.5	1274	15	US-10-282-122A-43837	Sequence 43837, A

ALIGNMENTS

RESULT 1

US-09-978-343-2
Sequence 2, Application US/09978343
Publication No. US20030082680A1

GENERAL INFORMATION:

APPLICANT: HOSTETTER, MARGARET K.

GALE, CHERYL A.

BENDER, CATHERINE M.

TAO, NIAN-JUN

KENDRICK, KATHLEEN

TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE

PROTEIN, ANTIBODIES, AND METHODS OF USE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORTING, RALPH, GERHARDT & SCHWAPPACH, P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MINNESOTA

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/978,343

FILING DATE: 15-Oct-2001

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/642,846

FILING DATE: 03-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: MORTING, ANN M.